


Exhibit 3



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Features: ☐ SNP ☐ CDD ☒ MGC ☒ HPRD ☐

☐ 1: [Z33381](#). Reports *T.reesei* (QM9414)...[gi:485863]

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LOCUS TRGE14BG 1124 bp DNA linear PLN 26-JUN-1995

DEFINITION T.reesei (QM9414) gene for endo-1,4-beta-glucanase.

ACCESSION Z33381

VERSION Z33381.1 GI:485863

KEYWORDS endo-1,4-beta-glucanase; endo-1,4-beta-glucanase V.

SOURCE Hypocrea jecorina

ORGANISM [Hypocrea jecorina](#)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE 1 (bases 1 to 1124)

AUTHORS Saloheimo,A., Henrissat,B., Hoffren,A.M., Teleman,O. and Penttila,M.

TITLE A novel, small endoglucanase gene, egl5, from Trichoderma reesei isolated by expression in yeast

JOURNAL Mol. Microbiol. 13 (2), 219-228 (1994)

PUBMED [7984103](#)

REFERENCE 2 (bases 1 to 1124)

AUTHORS Saloheimo,A.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-1994) Saloheimo A., VTT Biotechnology and Food Research, Espoo, Finland

FEATURES Location/Qualifiers

source 1..1124
/organism="Hypocrea jecorina"
/mol_type="genomic DNA"
/db_xref="taxon:51453"

CDS join(76..144,205..270,333..926)
/codon_start=1
/product="endo-1,4-beta-glucanase V (EGV)"
/protein_id="CAA83846.1"
/db_xref="GI:485864"
/db_xref="GOA:P43317"
/db_xref="UniProtKB/Swiss-Prot:P43317"
/translation="MKATLVLGSLIVGAVSAYKATTRYDYGQEGACGCGSSSGAFPW
QLGIGNGVYTAAGSQALFDTAGASWCGAGCGKCYQLTSTGQAPCSCGTGGAGQSII
VMVTNLCPNNGNAQWCPVVGGTNQYGYSHFDIMAQNEIFGDNVVVDFEPIACPQQA
SDWGTCLCVGQQETDPTPVLGNDTGSTPPGSSPPATSSSPSGGGQQTLYGQCGGAGW
TGPTTCQAPGTCKVQNQWYSQCLP"

mat_peptide join(127..144,205..270,333..923)
/gene="egl5"
/product="endo-1,4-beta-glucanase V (EGV)"
/EC_number="3.2.1.4"
/function="hydrolysis of beta-1,4-linkages in cellulose and beta-glucan"
/note="Based on hydrophobic cluster analysis, EGV belongs

to family K of cellulases/xylanases and family 45 of glycosyl hydrolases together with EGB of Pseudomonas fluorescens and EGV of Humicola insolens."

exon

76..144

/number=1

gene

join(127..144,205..270,333..923)

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intron

145..204

/gene="egl5"

/number=1

/cons_splice=(5'site:NO, 3'site:YES)

exon

205..270

/gene="egl5"

/number=2

intron

271..332

/gene="egl5"

/number=2

exon

333..923

/gene="egl5"

/number=3

misc_binding

813..923

/gene="egl5"

/bound_moiety="fungal cellulose"

ORIGIN

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gtaaccatcg

tgaccatgaa

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gttctcggct

ccctcattgt

aggcgccggt

121

tccgcgtaca

aggccaccac

cacggcaagt

ctacatgctt

ccaggtcaca

acgtctgctc

181

aacaacctct

aaccgaaagg

ccagcgctac

tacgatgggc

aggagggtgc

ttgcggatgc

241

ggctcgagct

ccggcgcat

cccgtggcag

gtaaacattc

gaccttgtct

ggggcaaggg

301

actcgtcact

tacatcctct

ctctctctgc

agctcggcat

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gtctacacgg

361

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601

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gagtcgcccg

tctggcggcg

gccagcagac

gctctatggc

cagtgtggag

841

gtgccggctg

gacgggacct

acgacgtgcc

aggccccagg

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gttcagaacc

901

agtggtaactc

ccagtgtctt

ccttgagaag

gccaagata

gccatgtctc

tctagcattc

961

ttccggcgtc

agtctgatct

gcctatttaa

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cattgctgct

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gcag

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